means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said position determining means;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said predicted exons and the DNA nucleotide sequence.

7. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

for reading data on at least one of the plurality of different DNA nucleotide sequences in said memory,

for predicting a plurality of different exons of said selected DNA nucleotide,

for storing the predicted exons in said memory,

for extracting a plurality of partial sequences meeting extraction conditions from said predicted exons and the data in said DNA nucleotide sequence, wherein said extraction conditions include a predetermined base length,

for determining positions of said plurality of partial sequences related to each one of said predicted exons and the DNA nucleotide sequence,

for selecting a plurality of different partial sequences from results of the determining step, and

for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences, and

for automatically collating said plurality of pairs of primers with said predicted exons and the DNA nucleotide sequence.

19. A primer design system, comprising:

means for selecting at least one DNA nucleotide sequence based on at least one predetermined genetic function of interest from a database having data on a plurality of DNA nucleotide sequences of the human genome;

means for predicting and storing a plurality of different exons of said selected DNA nucleotide; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting certain base length extraction conditions from the predicted exons;

means for determining positions of said plurality of partial sequences related to each one of said predicted exons and the DNA nucleotide sequence;

means for selecting a plurality of different partial sequences from said plurality of partial sequences; and

means for determining a plurality pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with said predicted exons and the DNA nucleotide sequence.

20. A primer design system, comprising:

means for selecting at least one DNA nucleotide sequence from a database including a plurality of DNA nucleotide sequences of the human genome;

means for predicting and storing a plurality of different exons of said selected DNA nucleotide; and

a control unit for controlling the system, said control unit controlling:

means for associating the predicted exons with corresponding regions in [each of] the DNA nucleotide sequence;

means for extracting a plurality of partial sequences from the predicted exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

means for collating positions of said plurality of partial sequences related to each of the predicted exons;

means for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences, wherein more than one partial sequence is associated with a genomic sequence;

means for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

means for automatically collating said plurality of pairs of primers with at least the positions related to said predicted exons and the DNA nucleotide sequence.

22. A storage medium having recorded thereon a program executable at a control unit in a computer with memory recording data on a plurality of different DNA nucleotide sequences of the human genome, said program comprising instructions

for reading data on at least one DNA nucleotide sequence in said memory;

for predicting a plurality of different exons of said selected DNA nucleotide;

for storing the predicted exons in the memory;

for positioning the predicted exons associated with genetic functions of interest on the DNA nucleotide sequence;

for extracting a plurality of partial sequences from the predicted exons under extraction conditions, wherein said extraction conditions include a predetermined base length;

for collating positions of said plurality of partial sequences related to each of the predicted exons and the genetic functions;

for selecting a plurality of different partial sequences from said plurality of partial sequences based on results of said means for collating positions of said plurality of partial sequences;

for determining a plurality of pairs of primers for normal PCR for each of said plurality of different partial sequences; and

for automatically collating said plurality of pairs of primers with at least the positions related to said predicted exons and the DNA nucleotide sequence.

Please add new claims as follows:

30.   A method for designing primers, comprising the steps of:

selecting at least one DNA nucleotide sequence from a database, said database including a DNA nucleotide sequence of the human genome;

predicting a plurality of exons of said selected DNA nucleotide using at least one exon predicting program;

extracting a partial sequence corresponding to each of said predicted exons meeting extraction conditions, wherein said extraction conditions include a base length; and

determining the primers for each of said extracted partial sequences.

31.   A method for designing primers according to claim 30, wherein said extraction conditions include a condition selected from the group consisting of GC contents, Tm, Tm, and combination thereof.

32.   A method for designing primers according to claim 30, further comprising the steps of:

after said extracting step, selecting at least one partial sequence from said extracted partial sequences based on the results of a homology search that utilizes said extracted partial sequences as a query.

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